

Gencore version 5.1.3
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

SUMMARIES

Run on: December 13, 2002, 20:59:48 ; Search time 2883 Seconds
(without alignments) 1655.519 Million cell updates/sec

Title: US-09-659-737a-1
Perfect score: 164
Sequence: 1 gcacccggacatcaaggcaq tgccctggatggccccaagaq 164

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenEmbl:*

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2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_cv:*

6: gb_pat:*

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3	152.8	93.2	3111	6	AX482007 AX482007 Sequence
4	152.8	93.2	3518	6	AX482009 AX482009 Sequence
5	149.6	91.2	3910	9	HS311797 Homo sapi
6	149.6	91.2	4667	9	AJ311798 Homo sapi
7	136.4	83	118632	9	AL133380 Human DNA
8	120.8	73.7	3616	10	BC021891 Mus muscu
9	106	64.6	168795	2	AC102420 Mus muscu
10	104.4	63.7	96101	2	AC112003 Rattus no
11	94.2	57.4	3931	9	AF251442 Homo Sapi
12	83	50.6	3531	9	HSU077470 Sequence
13	83	50.6	3558	9	AX399580 Sequence
14	83	50.6	3603	9	HOMMLK3A
15	83	50.6	3603	9	BC011263 Homo sapi
16	83	50.6	3799	9	AK092015 Homo sapi
17	82	50.0	166200	9	AC004816 Homo sapi
18	79.2	48.3	3951	5	AF154413 Fugu rubr
19	78.8	47.4	197943	2	AC125351 Mus muscu
20	78.8	48.0	203574	2	AC124595 Mus muscu
21	75	45.7	2390	10	BC030928 Mus muscu
22	73.4	43.8	3138	9	HENSTM R. sapiens M
23	73.4	44.8	3454	6	AX337845 Sequence
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25	72.8	44.1	150694	2	AP001459 Homo sapi
26	72.4	41.1	686	11	G33125 Epi0F7aS Hu
27	72.4	44.1	140356	2	AP000803 Homo sapi
28	72.4	44.1	162445	2	AC022488 Homo sapi
29	72.4	44.1	211382	9	AP001362 Homo sapi
30	72	43.9	404	6	I44517 Sequence 21
31	67.8	41.3	66251	2	AC00718 Mus muscu
32	66	40.2	3340	2	AC130251 Rattus no
33	64.8	39.5	168423	2	AC11962 Rattus no
34	64.4	39.3	46440	10	AC151542 Mus muscu
35	62.4	38.0	2139	9	AK090614 Homo sapi
36	62	37.8	137	6	I44513 Sequence 13
37	60	36.6	215615	2	AC074312 Mus muscu
38	60	36.6	226059	2	AC079488 Mus muscu
39	60	36.6	243275	2	AC073705 Mus muscu
40	59.8	36.5	10429	2	AC011486 Homo sapi
41	59.8	36.5	178335	9	AC118344 Homo sapi
42	58.4	35.6	170094	2	AC120811 Rattus no
43	57.4	35.0	3447	3	AF416233 Drosophili
44	57.4	35.0	5129	3	AY045717 Drosophili
45	57.4	35.0	5131	3	AY119549 Drosophili

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	
1	AX139125	Sequence 1 from Patent EP1085093.	AX139125	1	164 bp	DNA	linearity	PAT 30-MAY-2001

JOURNAL	Patent: EP 1085053-A 1-21-MAR-2001;
FEATURES	NEW YORK UNIVERSITY (US)
source	Location/Qualifiers
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RESULT 2	
AX207410	AX207410
LOCUS	Sequence 23 from Patent WO0155356.
DEFINITION	AX207410
JOURNAL	GI:15395228
VERSION	
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Bacteria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 2157)
TITLE	Plowman,G., Whyte,D., Manning,G., Sudarsanan,S. and Martinez,R.
JOURNAL	Human protein kinases and proteine kinase-like enzymes
PATENT	WO 0153556-A 23 02-AUG-2001;
Sugen, Inc. (US)	
FEATURES	Location/Qualifiers
source	1..2157 /organism="Homo sapiens" /db_xref="taxon:9606"
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AX208209	AX208209
LOCUS	AX482009
DEFINITION	Sequence 3 from Patent WO02055685.
ACCESSION	3518 bp
VERSION	DNA
KEYWORDS	linear
SOURCE	PAT 30-AUG-2001;
ORGANISM	Homo sapiens
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Bacteria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 Hu,Y., Kieke,J.A. and Donoho,G.
TITLE	Novel human kinase and polynucleotides encoding the same
JOURNAL	Patent: WO 02055685-A 3 18-JUL-2002;
FEATURES	Lexicon Genetics Incorporated (US)
source	Location/Qualifiers
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RESULT 5					RESULT 6
Locus	HSA311797	3910 bp	mRNA	linear	PRI 12-DEC-2001
DEFINITION	Homo sapiens mRNA for mixed lineage kinase 4alpha (MLK4ALPHA gene).				HSA311798
ACCESSION	AJ311797				HSN311798
VERSION	AJ311797.1	GI:1736728			4667 bp
KEYWORDS	mixed lineage kinase 4alpha; MLK4ALPHA gene.				mRNA
SOURCE					linear
ORGANISM	Homo sapiens				PRI 12-DEC-2001
AUTHORS	Krasha, S., Protopopov, A., Ryditch, A., Zabarovsky, E. and Kashuba, V.				
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Krasha, S., Protopopov, A., Ryditch, A., Zabarovsky, E. and Kashuba, V.				
TITLE	MLK4, a new member of mixed lineage kinases				
JOURNAL	Unpublished				
REFERENCE	2	(bases 1 to 3910)			
AUTHORS	Kashuba, V.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-APR-2001) Kashuba, V., Microbiology and Tumorbiology Center, Karolinska Institute, Box 280, 171 77, SWEDEN				
FEATURES					
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repeat_region	/note="20 copies 2 mer at 77% conserved"	16577	16638	
repeat_region	/note="LIM4 repeat: matches 2693. . 2784 of consensus"	16639	16726	
repeat_region	/note="AluX repeat: matches 24. . 288 of consensus"	16727	16889	
repeat_region	/note="LIM4 repeat: matches 2120. . 2375 of consensus"	16742	16763	
repeat_region	/note="LIMEC repeat: matches 2407. . 2364 of consensus"	18214	18422	
repeat_region	/note="LIMEC repeat: matches 6057. . 6144 of consensus"	18422	18740	
repeat_region	/note="AluJ repeat: matches 1. . 309 of consensus"	18741	19382	
repeat_region	/note="LIMEC repeat: matches 2311. . 2620 of consensus"	19580	19681	
repeat_region	/note="LIMB8 repeat: matches 6113. . 6174 of consensus"	19776	19948	
repeat_region	/note="LIME3 repeat: matches 2105. . 2311 of consensus"	20173	20579	
repeat_region	/note="MSTB repeat: matches 1. . 422 of consensus"	20631	20862	
repeat_region	/note="MIR repeat: matches 22. . 245 of consensus"	21161	21474	
repeat_region	/note="AluX repeat: matches 1. . 312 of consensus"	21772	21873	
repeat_region	/note="51 copies 2 mer aa 60% conserved"	2246	22531	
repeat_region	/note="AluX repeat: matches 1. . 289 of consensus"	22582	22894	
repeat_region	/note="AluX repeat: matches 1. . 311 of consensus"	23001	23421	
repeat_region	/note="LIM4 repeat: matches 2740. . 3046 of consensus"	23668	23548	
repeat_region	/note="MLT1J repeat: matches 104. . 191 of consensus"	23643	24023	
repeat_region	/note="MSTB repeat: matches 1. . 418 of consensus"	24596	24676	
query Match	83.2%	Score 136.4; DB 9; Length 118632;		
best Local Similarity	99.3%	Pred. No. 1.1e-29; Indels 0; Gaps 0;		
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	/lab_host="DHLB"			
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	FAMLRHENITOLRGYLRLPQHPLVILHDFGLKSNLLEHDICNUKIKI			
	QILVNNVAVOLAGMMVLEAWPVLHDFGLKSNLLEHDICNUKIKI			
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	59488 ATTGCGGTGTCGGAGGGATGGACAGGACACAAATGAGGAAGCTGAGCTG			
	59487 TTTGCTACTTGAGAGATAGAATGACATCTGCAATAAACACTTGAGATTACG			
	87 ATTCGGTGGCGAGGGATGGACAGGACACAAATGAGGAAGCTGAGCTG			
	146 MPOESFISMEDWKLPESTPCKTEKMRERSLRAOLQSOELURRQQL			
	59547 QASPTLKRSSDGSGLCSPPSPLMPMFRPLQLQSLDNKNTTRGRNMVQFQDFDKV			

23808 23907: gap of 100 bp
 * 23908 26130: contig of 2223 bp in length
 * 26131 26230: gap of 100 bp
 * 26231 28914: contig of 2744 bp in length
 * 28975 29074: gap of 100 bp
 * 29075 31408: contig of 2334 bp in length
 * 31409 31508: gap of 100 bp
 * 31509 35352: contig of 3844 bp in length
 * 35353 35452: gap of 100 bp
 * 35453 40317: contig of 4865 bp in length
 * 40318 40417: gap of 100 bp
 * 40418 40750: contig of 7033 bp in length
 * 47501 47600: gap of 100 bp
 * 47601 54652: contig of 7052 bp in length
 * 54653 54752: gap of 100 bp
 * 54753 67192: contig of 12440 bp in length
 * 67193 67292: gap of 100 bp
 * 80111 80111: contig of 12819 bp in length
 * 80112 80211: gap of 100 bp
 * 80212 94967: contig of 14756 bp in length
 * 94968 95067: gap of 100 bp
 * 95068 116109: contig of 21042 bp in length
 * 116110 116209: gap of 100 bp
 * 116210 13704: contig of 20795 bp in length
 * 137005 137104: gap of 100 bp
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 /db_xref="Taxon:10050"
 /clone_id="RPCI-24 Male Mouse BAC"
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 67293..80111

BASE COUNT 44905 a 38267 c 38200 g 45020 t 2403 others

Query Match 64.6%; Score 106; DB: 2; Length 168795;
 Best Local Similarity 85.5%; Pred NO. 1..1e-20;
 Matches 118; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Db 21384 TTTCGCTACTGTAGAGATAGACATGATGACATGCAATGAGCACAGCAGGGACATCAGG 21443
 QY 87 ATTTGGGTGGAGGAATGGCACAGGCCACCAAATGAGCACAGCAGGGACCTATG 146
 Db 21444 ACTTGGCTAGCGAGGGAAATGGCACAGGACCACAGGATGAGCCAGCAGGGACCTACG 21503
 QY 147 CCTGGATGGCCACAG 164
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FEATURES SOURCE
 /organism="Mus musculus"
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 /clone_id="RPCI-24 Male Mouse BAC"
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RESULT 10
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 LOCUS AC112003 96101 bp DNA LINEAR HTG 13-JUL-2002
 DEFINITION Rattus norvegicus clone CH230-234D24, *** SEQUENCING IN PROGRESS
 ***, 49 unorderd pieces.
 ACCESSION AC112003
 VERSION AC112003.2 GI:21737368
 KEYWORDS HTG; HTGS; PHASEI.

SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 Rattus;
 1 (bases 1 to 96101)
 REFERENCE (bases 1 to 96101)
 AUTHORS Muzny,D.M., Adams,C., Adio-oduola,B., Ali-osman,F.R., Allen,C.,
 Alshbrooks,S.L., Amaralunige,C., Are,J.R., Ayele,M., Banks,T.,
 Baranica,J., Benton,J., Blinige,K., Blankenburg,K., Bonin,D.,
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buahy,C., Burch,P., Burkett,K.L., Byrd,N.C.,
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 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Dunn,A.L., Ding,Y., Dinh,H.H.,
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 Wu, C., Wu, Y., Wu, Y.-F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstock, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 96101)
 Worley, K.C.
 Direct Submission
 Submitted (19-FEB-2002), Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 12, 2002 this sequence version replaced gi:18701953.
 ----- Genome Center of Medicine
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.edu>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: G0ZX
 Center clone name: CH230-234D24
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 49084 bases at least Q40
 Consensus quality: 53702 bases at least Q30
 Consensus quality: 57526 bases at least Q20
 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank/draft_data.html).
 * NOTE: This is a working draft sequence. It currently
 * consists of 49 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 2823: contig of 1360 bp in length
 4182: gap of unknown length
 4282: gap of unknown length
 4283: contig of 1656 bp in length
 5939: 6038: gap of unknown length
 6039: 7047: contig of 1009 bp in length
 7048: 7147: gap of unknown length
 7148: 8409: contig of 1262 bp in length
 8410: 8509: gap of unknown length
 8510: 8989: contig of 1380 bp in length
 9890: 9989: gap of unknown length
 9990: 11462: contig of 1473 bp in length
 11463: 11562: gap of unknown length
 11563: 12742: contig of 1180 bp in length
 12743: 12841: gap of unknown length
 12843: 13851: contig of 1009 bp in length
 13852: 13951: gap of unknown length
 13952: 15437: contig of 1486 bp in length
 15438: 15538: contig of 1589 bp in length
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 17227: 18632: contig of 1406 bp in length
 18633: 2036: gap of unknown length
 18733: 2046: contig of 1614 bp in length
 20347: 2045: contig of 1159 bp in length
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 21706: 22946: contig of 1244 bp in length
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 23050: 24436: contig of 1387 bp in length
 24437: 24536: gap of unknown length
 24537: 24637: contig of 1501 bp in length
 26038: 26138: contig of 2124 bp in length
 28261: 28262: gap of unknown length
 31453: 32528: contig of 1076 bp in length
 32229: 32628: gap of unknown length
 32629: 34558: contig of 1930 bp in length
 34559: 34687: gap of unknown length
 34687: 34752: contig of 1829 bp in length
 34752: 36587: gap of unknown length
 36587: 38910: contig of 2323 bp in length
 38911: 39010: gap of unknown length
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 40587: 41854: contig of 1306 bp in length
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 44350: 44449: contig of 2395 bp in length
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 46841: 479739: contig of 2395 bp in length
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 49639: 51158: contig of 1419 bp in length
 51158: 51258: gap of unknown length
 51258: 533004: contig of 1745 bp in length
 533004: 535104: gap of unknown length
 535104: 557785: contig of 2395 bp in length
 557785: 558848: gap of unknown length
 558848: 56449: contig of 256 bp in length
 56449: 58548: gap of unknown length
 58548: 60250: contig of 1702 bp in length
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 60351: 62643: gap of unknown length
 62643: 62742: gap of unknown length
 62742: 63903: contig of 1161 bp in length
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 64003: 66598: contig of 2595 bp in length
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 72704: 72705: contig of 2810 bp in length
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 78089: 78189: gap of unknown length
 78189: 79571: contig of 1382 bp in length
 79571: 79572: gap of unknown length
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 79672: 82116: gap of unknown length
 82116: 82217: gap of unknown length
 82217: 84149: contig of 2033 bp in length
 84149: 84150: gap of unknown length
 84150: 84250: contig of 3944 bp in length
 84250: 88193: gap of unknown length
 88193: 88194: contig of 3438 bp in length
 88194: 91732: gap of unknown length
 91732: 91831: contig of 3438 bp in length

FEATURES	*	91832	96101: contig of 4270 bp in length.
SOURCE	Location/Qualifiers		RDPGEPRLDPPNVPFPFPRRWNTQDSSLERPLRPRPSANQRQRLDPWWFW SPSHARSTSPTRANSSTETRNLDCAFASSTSVFPRGFLPALLPQAGLPPTERTL DLDAQSQSDTYPICRAELNTHPAPYEQEWFs
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BASE COUNT	23908	a 21808 c 22462 g 23062 t 4861 others	ORIGIN
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Query Match	63.7%	Score 104.4; DB 2;	Length 96101;
Best Local Similarity	84.8%	Pred. No. 3.2e-20;	
Matches	117;	Conservative 0; Mismatches 21;	Indels 0; Gaps 0;
VERSION	AF251442.1	GI:12005723	
KEYWORDS	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 3931)		
AUTHORS	Mcnee,J.J., Dower,S.K. and Guesdon,F.		
TITLE	cDNA sequence and gene organisation of mixed lineage kinase 1		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3931)		
AUTHORS	Mcnee,J.J. and Guesdon,F.		
JOURNAL	Submitted (03-APR-2000) Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Glossop Road, Sheffield S10 2JF, United Kingdom		
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ORIGIN			
Query Match	57.4%	Score 94.2; DB 9;	Length 3931;
Best Local Similarity	73.6%	Pred. No. 2.7e-17;	
Matches	120;	Conservative 0; Mismatches 43;	Indels 0; Gaps 0;
VERSION			
KEYWORDS			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
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BASE COUNT	875	a 1153 c 1134 g 769 t	ORIGIN
ORIGIN			
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Best Local Similarity	73.6%	Pred. No. 2.7e-17;	
Matches	120;	Conservative 0; Mismatches 43;	Indels 0; Gaps 0;
VERSION			
KEYWORDS			
ORGANISM			
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source			
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misc_feature	/note="sprk"	Best Local Similarity	Score	Best Local Similarity	Score	Best Local Similarity	Score
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	/note="32 A residues"						
BASE COUNT	635	a	1207	c	1143	g	549
ORIGIN	635	a	1211	c	1161	g	551
RESULT	14						
HUMMLK3A							
LOCUS	RUMMLK3A						
DEFINITION	Human protein kinase (MLK-3) mRNA, complete cds.						
ACCESSION	U32975						
VERSION	L32975.1						
KEYWORDS	MLK-3 gene; protein kinase.						
SOURCE	Homo sapiens (tissue library: lambda gt10) thymus cDNA to mRNA.						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	1 (bases 1 to 3558)						
TITLE	Ingl, I.L., Leung, I.W., Heng, H.H., Tsui, L.C. and Lassam, N.J.						
JOURNAL	MLK-3: identification of a widely-expressed protein kinase bearing						
PUBMED	an SH3 domain and a leucine zipper-basic region domain						
FEATURES	Oncogene 9 (6), 1745-1750 (1994)						
SOURCE	94239754						
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BASE COUNT 635 a 1211 c 1161 g 551 t

ORIGIN

Query Match 50.6%; Score 83; DB 9; Length 3558;
Best Local Similarity 69.3%; Pred. No. 5.6e-14; Matches 113; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Accession 2 CACGGGACATCAAGCGGAATAATTGCTCTTGAGAGTAGAACATGAGACATC 61
Db 1196 CACCGTGACTCAAGTCACACATTTGCTCTGAGAGTAGAGACATC 61
Qy 62 TGCATAAACTTGAGATTACAGATTGGTTGGGGATGGCACAGGACCC 121
Db 1256 GACCAAGAACCTTGAGATCACGACTTGCGCTGGCCGAGATGGCACAAACCACA 1315
Qy 122 AAAATGAGCACAGGGACCTATGCCCTGATGGCTCTGGAGG 164
Db 1316 CAATGAGTGCCGGGACCTACGCCCTGATGGCTCTGGAGG 1358

CDS

RESULT 15
BC011263 BC011263 3603 bp mRNA linear PRI 30-JUL-2001
DEFINITION Homo sapiens, Similar to mitogen-activated protein kinase kinase 11, clone MGC:17114 IMAGE:4215281, mRNA, complete cds.
ACCESSION BC011263 VERSION BC011263.1 GI:15030036
KEYWORDS MGC.
SOURCE
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 3603)
AUTHORS Strauberg, R.
TITLE Direct Submission
JOURNAL Submitted(25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA
REMARK NIH-MGC Project URL: http://mgc.ncbi.nih.gov
COMMENT Contact: MGC help desk
Email: cgps@nih.nih.gov
Tissue Procurement: David N Louis, M.D.
Center code: BCM_HGSC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)
Sequencing Center
Center code: BCM_HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Huiyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov Series: ITRAK Plate: 12 Row: o Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505194. Location/Qualifiers 1. -3603 /organism="Homo sapiens"
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CDS

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ACCESSION BC011263 VERSION BC011263.1 GI:15030036
KEYWORDS MGC.
SOURCE
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 3603)
AUTHORS Strauberg, R.
TITLE Direct Submission
JOURNAL Submitted(25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA
REMARK NIH-MGC Project URL: http://mgc.ncbi.nih.gov
COMMENT Contact: MGC help desk
Email: cgps@nih.nih.gov
Tissue Procurement: David N Louis, M.D.
Center code: BCM_HGSC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)
Sequencing Center
Center code: BCM_HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Huiyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.

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Db 1208 CACCGTGACTCAAGTCACACATTTGCTCTGAGAGTAGAGACATC 61
Qy 62 TGCATAAACTTGAGATTACAGATTGGTTGGCGAGGGATGGCACAGGACCC 121
Db 1268 GACCAAGAACCTTGAGATCACGACTTGCCCGCCGAGATGGCACAAACCACA 1370
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Db 1328 CAATGAGTGCCGGGGACCTACGCCCTGGATGGCTCCIGAG 1370

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